FILE 'USPATFULL' ENTERED AT 16:36:54 ON 26 AUG 2003
L4 2 S (((GENOME OR CHROMOSOMAL) (W)REARRANGEMENT) AND DISEASE)/CLM

=> d 2 bib,kwic

L4 ANSWER 2 OF 2 USPATFULL on STN
AN 2002:262200 USPATFULL
TI Triplex in-situ hybridization
IN Fresco, Jacques R., Princeton, NJ, United States
Johnson, Marion D., East Windsor, NJ, United States
PA Princeton University, Princeton, NJ, United States (U.S. corporation)
PI US 6461810 B1 20021008
WO 9924622 19990520
AI US 2000-531000 20000908 (9)
WO 1998-US23765 19981110
20000908 PCT 371 date
PRAI US 1997-64997P 19971110 (60)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Wortman, Donna
LREP Rothwell, Figg, Ernst & Manbeck, p.c.
CLMN Number of Claims: 26
ECL Exemplary Claim: 1
DRWN 14 Drawing Figure(s); 7 Drawing Page(s)
LN.CNT 1334
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
CLM What is claimed is:
. . . third strand is designed to allow detection of extra or missing chromosomes, extra or missing portions of a chromosome, or **chromosomal rearrangements**.

21. The method of claim 1, wherein the method is used to screen individuals at risk for developing a **disease**.

22. The method of claim 1, wherein the method is diagnostic of an infectious **disease**.

(FILE 'HOME' ENTERED AT 16:27:54 ON 26 AUG 2003)

FILE 'MEDLINE' ENTERED AT 16:28:06 ON 26 AUG 2003
L1 326 S ((GENOME OR CHROMOSOMAL) (W)REARRANGEMENT) AND DISEASE
L2 24 S L1 AND REVIEW
L3 86 S L1 AND REVIEW/DT

=> d bib, abs 33,34,37,43,44,51,52,53,54,57,70,71,73,80

L3 ANSWER 33 OF 86 MEDLINE on STN
AN 2000311374 MEDLINE
DN 20311374 PubMed ID: 10851249
TI Perfect endings: a review of subtelomeric probes and their use in clinical diagnosis.
AU Knight S J; Flint J
CS Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford OX3 9DS, UK.
SO JOURNAL OF MEDICAL GENETICS, (2000 Jun) 37 (6) 401-9. Ref: 65
Journal code: 2985087R. ISSN: 1468-6244.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 200008
ED Entered STN: 20000811
Last Updated on STN: 20020125
Entered Medline: 20000802
AB **Chromosomal rearrangements** involving the ends of chromosomes (telomeres) are emerging as an important cause of human genetic **diseases**. This review describes the development of first and second generation sets of telomere specific clones, together with advances in fluorescence in situ hybridisation (FISH) technology, which have made the prospect of screening for telomeric rearrangements a realistic goal. Initial FISH studies using the telomere specific clones indicate that they will be a valuable diagnostic tool for the investigation of mental retardation, the characterisation of known abnormalities detected by conventional cytogenetic analysis, spontaneous recurrent miscarriages, infertility, haematological malignancies, and preimplantation diagnosis, as well as other fields of clinical interest. In addition, they may help investigate telomere structure and function and can be used in the identification of dosage sensitive genes involved in human genetic **disease**.

L3 ANSWER 34 OF 86 MEDLINE on STN
AN 2000232004 MEDLINE
DN 20232004 PubMed ID: 10767636
TI Recurrent chromosome aberrations in cancer.
AU Mitelman F
CS Department of Clinical Genetics, University Hospital, SE-221 85, Lund, Sweden.. felix.mitelman@klingen.lu.se
SO MUTATION RESEARCH, (2000 Apr) 462 (2-3) 247-53. Ref: 23
Journal code: 0400763. ISSN: 0027-5107.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 200006
ED Entered STN: 20000629
Last Updated on STN: 20000629

Entered Medline: 20000616

AB Cytogenetic investigations of neoplastic cells during the past 25 years have revealed more than 600 acquired, recurrent, balanced chromosome rearrangements, and it has been established that every tumor type, studied in a sufficient number to permit conclusions, may be subdivided on the basis of specific, and even pathognomonic, abnormalities. At the molecular level, the balanced rearrangements exert their action through one of two alternative mechanisms: Deregulation of one gene by relocation to an immunoglobulin or T-cell receptor gene, or the creation of a hybrid gene by the fusion of parts of two genes. At present, nearly 100 genes have been found to be involved in neoplasia-associated **chromosomal rearrangements**, the great majority in hematological disorders. At the same time, the clinical usefulness of various cytogenetic abnormalities as diagnostic and prognostic aids has been increasingly appreciated. The identification of a recurring chromosome abnormality can assist in the diagnosis and subclassification of a malignant **disease** and, hence, in the selection of the appropriate treatment. The karyotype is also an independent prognostic factor. In hematological neoplasms, where the knowledge of chromosome abnormalities still is much more complete than is the case with solid tumors, cytogenetic analysis now plays an integral part in the diagnostic work-up of individual patients. Data obtained during recent years strongly suggest that corresponding breakthroughs will be achieved in solid tumors within a not-too-distant future.

L3 ANSWER 37 OF 86 MEDLINE on STN
AN 1999221295 MEDLINE
DN 99221295 PubMed ID: 10206454
TI **Chromosomal rearrangements** in childhood acute myeloid leukemia and myelodysplastic syndromes.
AU Martinez-Climent J A; Garcia-Conde J
CS Department of Hematology and Oncology, Hospital Clinico Universitario, University of Valencia, Spain.
SO JOURNAL OF PEDIATRIC HEMATOLOGY/ONCOLOGY, (1999 Mar-Apr) 21 (2) 91-102. Ref: 182
Journal code: 9505928. ISSN: 1077-4114.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LA English
FS Priority Journals
EM 199904
ED Entered STN: 19990517
Last Updated on STN: 19990517
Entered Medline: 19990430

AB Recurrent chromosomal abnormalities present in the malignant cells of children with acute myeloid leukemia (AML) and myelodysplastic syndromes (MDS) often correlate closely with specific clinical and biologic characteristics of the **disease**. Certain unique cytogenetic rearrangements are associated with distinct morphologic leukemic subtypes. These rearrangements should be detectable in most children with AML and MDS with the use of complementary molecular techniques such as fluorescence in situ hybridization (FISH), Southern blotting, and polymerase chain reaction. Apart from the diagnostic assessment, cytogenetic findings sometimes predict clinical outcome and thus also serve as prognostic parameters, which may affect the therapeutic decision. Alternative classifications of AML that take into account the genetic information are being proposed. Cytogenetic and molecular analyses may allow clinicians to more appropriately direct types of treatment. Abnormal fusion transcripts and chimeric proteins derived from karyotypic abnormalities now are being also targeted by novel therapeutic approaches.

L3 ANSWER 43 OF 86 MEDLINE on STN

AN 1998407943 MEDLINE
DN 98407943 PubMed ID: 9735383
TI Chromosome painting: a useful art.
AU Ried T; Schrock E; Ning Y; Wienberg J
CS National Human Genome Research Institute, National Institutes of Health, Building 49, Room 4A28, 49 Convent Drive, Bethesda, MD 20892-4470, USA.. tried@nhgri.nih.gov
SO HUMAN MOLECULAR GENETICS, (1998) 7 (10) 1619-26. Ref: 90
Journal code: 9208958. ISSN: 0964-6906.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199811
ED Entered STN: 19990106
Last Updated on STN: 19990106
Entered Medline: 19981116
AB Chromosome 'painting' refers to the hybridization of fluorescently labeled chromosome-specific, composite probe pools to cytological preparations. Chromosome painting allows the visualization of individual chromosomes in metaphase or interphase cells and the identification of both numerical and structural chromosomal aberrations in human pathology with high sensitivity and specificity. In addition to human chromosome-specific probe pools, painting probes have become available for an increasing range of different species. They can be applied to cross-species comparisons as well as to the study of **chromosomal rearrangements** in animal models of human **diseases**. The simultaneous hybridization of multiple chromosome painting probes, each tagged with a specific fluorochrome or fluorochrome combination, has resulted in the differential color display of human (and mouse) chromosomes, i.e. color karyotyping. In this review, we will summarize recent developments of multicolor chromosome painting, describe applications in basic chromosome research and cytogenetic diagnostics, and discuss limitations and future directions.

L3 ANSWER 44 OF 86 MEDLINE on STN
AN 1998407942 MEDLINE
DN 98407942 PubMed ID: 9735382
TI Position effect in human genetic **disease**.
AU Kleinjan D J; van Heyningen V
CS MRC Human Genetics Unit, Western General Hospital, Crewe Road, Edinburgh EH4 2XU, UK.
SO HUMAN MOLECULAR GENETICS, (1998) 7 (10) 1611-8. Ref: 85
Journal code: 9208958. ISSN: 0964-6906.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199811
ED Entered STN: 19990106
Last Updated on STN: 19990106
Entered Medline: 19981116
AB The spatially, temporally and quantitatively correct expression of a gene requires the presence not only of intact coding sequence, free of adverse nucleotide changes, but also correctly functioning regulatory control. With the identification of an increasing number of **disease** -related genes, the molecular defect in many cases has been defined. It is becoming clear that it is not always the transcription unit that bears the defect: there are a number of cases where the regulation of gene expression has been compromised. Cases associated with

chromosomal rearrangement outside the transcription and promoter regions are categorized as position effects. A number of different mechanisms may explain their aetiology. Here, we examine the human disorders where such position effects are implicated. Further study of such cases may lead to important insights into mechanisms of gene regulation and transcriptional control.

L3 ANSWER 51 OF 86 MEDLINE on STN
AN 97234075 MEDLINE
DN 97234075 PubMed ID: 9118473
TI Genetic disorders of cardiac morphogenesis. The DiGeorge and velocardiofacial syndromes.
CM Comment in: Circ Res. 1997 Apr;80(4):604-6
AU Goldmuntz E; Emanuel B S
CS Division of Cardiology, University of Pennsylvania, Philadelphia, USA.
NC DC-02027 (NIDCD)
HD-26979 (NICHD)
HL-51533 (NHLBI)
+
SO CIRCULATION RESEARCH, (1997 Apr) 80 (4) 437-43. Ref: 64
Journal code: 0047103. ISSN: 0009-7330.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199704
ED Entered STN: 19970506
Last Updated on STN: 19980206
Entered Medline: 19970424
AB The phenotype associated with a 22q11 deletion is highly variable and still under investigation. Of particular interest to cardiologists and cardiac developmental biologists is the finding that many patients with a 22q11 deletion have conotruncal cardiac defects and aortic arch anomalies. Despite the phenotypic variability, the vast majority of patients have a similar large deletion spanning approximately 2 megabases. The low-frequency repeated sequences at either end of the commonly deleted region may be responsible for the size of the deletion and account for the instability of this chromosomal region. Molecular studies of patients with the DGS/VCFS phenotype and unique **chromosomal rearrangements** have allowed a minimal critical region for the **disease** to be defined. Multiple genes have been identified in the minimal critical and larger deleted region. These genes are being investigated for their potential role in the **disease** pathophysiology by screening for mutations in nondeleted patients with the phenotype and by analysis of the pattern of expression in the developing mouse embryo. Further experimentation in the mouse mammalian model system will be of great utility to help determine whether haploinsufficiency of one critical gene or several genes within the DGCR results in the **disease** phenotype. Modifying factors, both genetic and environmental, must also be considered. Further investigation into the **disease** mechanism leading to the DGS/VCFS phenotype will hopefully further our understanding of cardiac development and **disease**.

L3 ANSWER 52 OF 86 MEDLINE on STN
AN 97148035 MEDLINE
DN 97148035 PubMed ID: 9125323
TI Current status of the human malformation map.
AU Carey J C; Viskochil D H
CS Department of Pediatrics, University of Utah Health Sciences Center, Salt Lake City 84112, USA.
SO BIRTH DEFECTS ORIGINAL ARTICLE SERIES, (1996) 30 (1) 13-34. Ref: 149
Journal code: 0003403. ISSN: 0547-6844.

CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LA English
FS Priority Journals
EM 199704
ED Entered STN: 19970506
Last Updated on STN: 19970506
Entered Medline: 19970421
AB The recent advances in recombinant DNA technology are now being applied to map and clone the genes for dysmorphic syndromes. The genes for almost 40% of the malformation and dysplasia syndromes listed in Smith's Recognizable Patterns of Human Malformation [Jones, 1988] have now been mapped and/or identified. This strategy has dramatically changed the way in which clinical geneticists look at the basic mechanisms of genetic disorders. The primary purpose of applying positional cloning to human **disease**, including malformation syndromes, is to use the cloned gene to understand the basic pathogenesis of the disorder at hand. The importance of the application of knowledge of mouse models, to human molecular biology and the significance of the role of the clinician in documenting astute observations that assist in mapping cannot be overemphasized. Many of the successful outcomes in gene cloning in dysmorphic syndromes that have occurred thus far were clearly helped by the recognition of patients with **chromosomal rearrangements**. Collaboration of molecular biologists and clinical geneticists will clearly lead to the continued elucidation of the map location and cloned gene of many other disorders.

L3 ANSWER 53 OF 86 MEDLINE on STN
AN 97071955 MEDLINE
DN 97071955 PubMed ID: 8914800
TI Molecular diagnosis of lymphoma.
AU Veronese M L; Schichman S A; Croce C M
CS Thomas Jefferson Medical College, Kimmel Cancer Center, Philadelphia, PA 19107, USA.
SO CURRENT OPINION IN ONCOLOGY, (1996 Sep) 8 (5) 346-52. Ref: 44
Journal code: 9007265. ISSN: 1040-8746.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199702
ED Entered STN: 19970305
Last Updated on STN: 19970305
Entered Medline: 19970218
AB The biologic and clinical heterogeneity of lymphomas represents the major obstacle to their diagnosis. Because histologic analysis, which is the initial diagnostic approach, has been demonstrated to be insufficient in the definition of certain types of lymphomas, molecular and immunologic techniques have been increasingly applied to obtain a precise diagnosis and to establish a correct treatment. Fluorescence in situ hybridization, in particular, is a powerful technique with many applications to the study of **chromosomal rearrangements**. In addition, because of their specificity and sensitivity, molecular techniques provide an important tool in assessing response to treatment, in detecting minimal residual **disease**, and in understanding the clinical and prognostic significance of the **disease**.

L3 ANSWER 54 OF 86 MEDLINE on STN
AN 97063398 MEDLINE
DN 97063398 PubMed ID: 8907265

TI Non-random **chromosomal rearrangements** and their implications in clinical features and outcome of multiple myeloma and plasma cell leukemia.
AU Taniwaki M; Nishida K; Ueda Y; Takashima T
CS Third Department of Internal Medicine, Kyoto Prefectural University of Medicine, Japan.
SO LEUKEMIA AND LYMPHOMA, (1996 Mar) 21 (1-2) 25-30. Ref: 39
Journal code: 9007422. ISSN: 1042-8194.
CY Switzerland
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199703
ED Entered STN: 19970407
Last Updated on STN: 19970407
Entered Medline: 19970325
AB Rearrangements of bands 14q32.3 and 19p13.3 and preferential deletion of the short arm of chromosome 1 were nonrandom chromosomal abnormalities in MM and PCL, warranting further investigation at the molecular level. From the viewpoint of clinical relevance, chromosome 14q32 translocation seems to be associated with leukemic manifestation, level of LDH, and shorter survival period from the time of chromosomal analysis. However, these results were obtained from patients with advanced **disease**, most of whom had already been treated with alkylating agents prior to cytogenetic analysis. To investigate the karyotypes of MM in the early stage and to determine correlations with clinical features, non-dividing cells should be analyzed. For this purpose, interphase FISH and/or comparative genomic hybridization are promising procedures to detect genomic alterations in early multiple myeloma.

L3 ANSWER 57 OF 86 MEDLINE on STN
AN 96342101 MEDLINE
DN 96342101 PubMed ID: 8745068
TI Comparative maps: the mammalian jigsaw puzzle.
AU Eppig J T; Nadeau J H
CS Jackson Laboratory, Bar Harbor, ME 04609, USA.. jte@informatics.jax.org
NC HG 00330 (NHGRI)
SO CURRENT OPINION IN GENETICS AND DEVELOPMENT, (1995 Dec) 5 (6) 709-16.
Ref: 52
Journal code: 9111375. ISSN: 0959-437X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199610
ED Entered STN: 19961022
Last Updated on STN: 19980206
Entered Medline: 19961010
AB **Chromosomal rearrangements** such as inversions and translocations have played an important role in defining genome organization in existing mammals. The number of rearrangements that have occurred since divergence from the 'primordial' mammal has been modest and the distribution of these rearrangements among chromosomes seems to be random. As a result, each mammalian species has a unique arrangement of conserved and disrupted chromosomal segments as compared to other mammalian species. Genes are excellent markers for these chromosomal segments because homologies can be detected in highly divergent species. By comparing the chromosomal location of homologous genes in different species, maps of conserved chromosomal segments can be obtained. These comparative maps can be used to predict gene locations in other species,

identify candidate **disease** genes, characterize the genetic basis for complex traits, and find modulators of **disease** susceptibility. Equally important is the use of comparative maps for addressing questions about genome organization and evolution.

L3 ANSWER 70 OF 86 MEDLINE on STN
AN 91320260 MEDLINE
DN 91320260 PubMed ID: 1862441
TI The genetic basis of cancer.
AU Goldberg Y P; Parker M I; Gevers W
CS Department of Medical Biochemistry, University of Cape Town.
SO SOUTH AFRICAN MEDICAL JOURNAL, (1991 Jul 20) 80 (2) 99-104. Ref: 56
Journal code: 0404520. ISSN: 0038-2469.
CY South Africa
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LA English
FS Priority Journals
EM 199108
ED Entered STN: 19910922
Last Updated on STN: 19910922
Entered Medline: 19910830
AB Cancer is essentially a genetic **disease** resulting from congenital or acquired alterations in some cells of the patient. Such changes may occur in particular oncogenes and are responsible for the tumour phenotype of the affected population of cells. Oncogenes function by continuous positive action in the mitogenic pathway, and may become activated by point mutations, **chromosomal rearrangements**, gene amplification or viral insertion events. In contrast, unaltered tumour-suppressor genes are responsible for suppressing the neoplastic phenotype, and their inactivation by deletion or mutation permits cancerous development in the affected cells. The genetic model of carcinogenesis is thus based on the idea that mutations at the DNA level create a functional imbalance between the oncogenes and the tumour-suppressor genes, resulting in uncontrolled clonal proliferation. It is likely that the clinical importance of these recent findings will soon be realised and utilised in the development of therapies and diagnostic procedures that will directly benefit the patient.

L3 ANSWER 71 OF 86 MEDLINE on STN
AN 91187043 MEDLINE
DN 91187043 PubMed ID: 2011136
TI The segregation of cancer-causing genes in human populations.
AU Schull W J
CS University of Texas Health Science Center, Genetics Center, Houston 77225.
SO MUTATION RESEARCH, (1991 Apr) 247 (2) 191-8. Ref: 42
Journal code: 0400763. ISSN: 0027-5107.
CY Netherlands
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199105
ED Entered STN: 19910526
Last Updated on STN: 19910526
Entered Medline: 19910508
AB Cancer can arise through genetic damage of a variety of sorts, including recessive and dominant mutations, large **chromosomal rearrangements**, and the inability of cells to repair damaged DNA. Many of these events can be studied by standard methods of genetic analysis and thereby furnish the means to localize the gene to a specific region in the human genome. However, conventional methods of segregation

analysis cannot provide the molecular and cellular understanding of the process of gene action essential to informed intervention. Here, recent advances in molecular biology, immunology and biochemistry hold promise of providing the understanding of how normal cells control their replication and why cancer cells do not. Heretofore these techniques have been largely restricted to modest-sized studies, but the requisite assays have now reached a level of development that makes practicable large clinical and population-based studies. Collectively, through these rapidly evolving techniques, we may eventually achieve the acquisition of new methods of prevention, diagnosis and therapy, and a better awareness of the events that order the lives of our cells.

L3 ANSWER 73 OF 86 MEDLINE on STN
AN 91029278 MEDLINE
DN 91029278 PubMed ID: 2224917
TI Chromosome abnormalities in cancer.
AU Mitelman F; Heim S
CS Department of Clinical Genetics, University Hospital, Lund, Sweden.
SO CANCER DETECTION AND PREVENTION, (1990) 14 (5) 527-37. Ref: 50
Journal code: 7704778. ISSN: 0361-090X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199012
ED Entered STN: 19910208
Last Updated on STN: 20020125
Entered Medline: 19901207
AB Karyotypic abnormalities have been described in more than 10,000 human neoplasms analyzed by means of chromosome banding. These aberrations are of three different kinds: primary abnormalities, which are essential in establishing the tumor; secondary abnormalities, which develop only after the neoplasm is established but which nevertheless may be important in tumor progression; and cytogenetic noise, which is the background level of nonconsequential aberrations. These latter changes are, in contrast to the primary and secondary aberrations, randomly distributed throughout the genome. The primary abnormalities, of which more than 100 have been identified, are strictly correlated with particular neoplastic disorders and even with histopathological subgroups within a given tumor type. To these purely cytogenetic data implicating specific genetic changes in carcinogenesis may now be added the growing evidence of molecular specificity emerging from recombinant DNA studies. It appears that both currently known classes of directly cancer-relevant genes, the dominant oncogenes and the recessive anti-oncogenes, are located at precisely those genomic sites that are visibly involved in neoplasia-associated **chromosomal rearrangements**. The molecular genetic data thus support the cytogenetic conclusion that the distribution of consistently cancer-associated breakpoints reflects the genomic position of genes that, either directly or through the control function they exert, are essential in the proliferation and differentiation of human cells.

L3 ANSWER 80 OF 86 MEDLINE on STN
AN 88037425 MEDLINE
DN 88037425 PubMed ID: 3312830
TI New structural **chromosomal rearrangements** in congenital leukemia.
AU Heim S; Bekassy A N; Garwicz S; Heldrup J; Wiebe T; Kristoffersson U; Mandahl N; Mitelman F
CS Department of Clinical Genetics, University Hospital, Lund, Sweden.
SO LEUKEMIA, (1987 Jan) 1 (1) 16-23. Ref: 50
Journal code: 8704895. ISSN: 0887-6924.
CY United States

DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW OF REPORTED CASES)
LA English
FS Priority Journals
EM 198712
ED Entered STN: 19900305
Last Updated on STN: 20020125
Entered Medline: 19871207
AB The karyotypic abnormalities and clinical data on three patients in whom acute leukemia was diagnosed within the first 6 months of life are presented. The four structural **chromosomal rearrangements** detected in the bone marrow from these patients, i.e., t(7;12)(q36;p13) and t(1;19)(q11;q11) in case 1, t(2;10;11;12)(q21q31;p13;q13;q24) in case 2, and t(11;19)(q23;p13) in case 3, have not previously been associated with congenital leukemia. Acquired chromosomal changes have until now been reported in only 31 leukemic infants in this age group. Of the total material, 18 patients had acute lymphoblastic leukemia and 16 had acute nonlymphocytic leukemia. The by far most frequently recorded cytogenetic aberration has been t(4q;11q), seen in 14 cases of lymphoblastic leukemia. Although t(4q;11q) has not been found in a single patient with acute nonlymphocytic leukemia, these leukemias have often had other rearrangements involving the same region of 11q. Hence, genetic material around 4q21 may be active in lymphocytic differentiation, whereas gene(s) in 11q23 may be important in the neoplastic process in a less cell-type specific manner and perhaps particularly vulnerable to neoplastic rearrangement in fetal life. The finding of four cases out of 34 with translocations between 11q23 and chromosome 19 indicates that this rearrangement might characterize a specific cytogenetic subgroup of leukemia in the very young.